

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

In re application of

Confirmation No. 2875

Naoki MIDOH et al.

Attorney Docket No. 2002 0317A

Serial No.10/070,387

Group Art Unit 1652

Filed March 6, 2002

Examiner David J. STEADMAN

CYCLIC DEPSIPEPTIDE SYNTHETASE AND METHOD FOR RECOMBINANT PRODUCTION (as amended) Mail Stop: Appeal Brief - Patents

RESPONSE TO NOTIFICATION OF NON-COMPLIANT APPEAL BRIEF

Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

Sir:

In response to the Notification of Non-Compliant Appeal Brief dated July 25, 2006, enclosed herewith is a substitute Appeal Brief.

The substitute Appeal Brief has been revised to indicate "NONE" in the Related Proceedings Appendix on page 21 of the Brief as required by items 9-10 of the Notification.

A copy of the Notification is also enclosed herewith.

Favorable reconsideration is respectfully requested.

Respectfully submitted,

THE COMMISSIONER IS AUTHORIZED TO CHARGE ANY DEFICIENCY IN THE FEES FOR THIS PAPER TO DEPOSIT ACCOUNT NO. 23-0975

Naoki MIDOH et al.

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ATTACHMENTS

- 1. Substitute Appeal Brief; and
- 2. Copy of the Notification of Non-Compliant Appeal Brief.



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APPEAL BRIEF

Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

Sir:

This is an appeal from the final decision of the Examiner set forth in the final Office Action dated October 6, 2005, finally rejecting claims 13 and 15, which are attached herewith in the Claims Appendix. A Notice of Appeal was filed on March 6, 2006. A petition for a two month Extension of time hereby accompanies this Brief.

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Attorney Docket No. 2002_0317A Serial No. 10/070,387

August 25, 2006

I. REAL PARTY IN INTEREST

The real party in interest is MEIJI SEIKA KAISHA, LTD., assignee of the entire right, title and interest to this application.

II. RELATED APPEALS AND INTERFERENCES

There are no related prior nor pending appeals, interferences, or judicial proceedings known to Appellants, Appellants' legal representatives, or assignee which will affect or be affected by, or have a bearing on the Board's decision in the present appeal.

III. STATUS OF CLAIMS

The status of the claims as indicated in the Advisory Action dated January 27, 2006 is as follows:

Claims pending: 1-13 and 15

Claims withdrawn: 2-12

Claims rejected: 13 and 15

Claims in condition for allowance: 1

Claims appealed: 13 and 15

IV. STATUS OF AMENDMENTS

The last amendment to the claims was in the after final response filed on January 4, 2006. In item 7(b) on page 1 of the Advisory Action dated January 27, 2006, it was indicated that this amendment will be entered for purposes of Appeal.

V. SUMMARY OF THE CLAIMED SUBJECT MATTER

The invention of claim 1 relates to a novel cyclic depsipeptide synthetase polypeptide, which is a protein comprising the amino acid sequence of SEQ ID NO: 2. Support can be found at page 3, lines 16-19 of the disclosure. The claimed protein has cyclo(D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl-D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl) (PF1022) synthetase activity. See page 1, lines 13-17. The claimed protein has 3210 amino acid residues. See page 15, lines 16-24.

The invention of claim 15 is an isolated protein encoded by a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2; (b) the nucleotide sequence of SEQ ID NO: 1; (c) a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions at 0.2 x SSC concentration (1 x SSC: 15 mM trisodium citrate, 150 mM sodium chloride) in a 0.1 % SDS solution at 60 °C for 15 minutes and which encodes a protein having PF1022 synthetase activity; and (d) a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1 and which encodes a protein having PF1022 synthetase activity.

The invention of claim 13 relates to a method for producing the cyclic depsipeptide synthetase protein of SEQ ID NO: 2 having PF1022 synthetase activity. The method comprises: (1) culturing a host cell transformed with a vector containing a nucleotide sequence under conditions suitable for protein expression, wherein the nucleotide sequence is selected from the group consisting of: (a) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2; (b) the nucleotide sequence of SEQ ID NO: 1; (c) a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions at 0.2 x SSC concentration (1 x SSC: 15 mM trisodium citrate, 150 mM sodium chloride) in a 0.1 % SDS solution at 60 °C for 15 minutes and which encodes a protein having PF1022 synthetase activity; and (d) a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1

and which encodes a protein having PF1022 synthetase activity; and (2) collecting the protein from the culture medium.

Support for elements (a) and (b) of claims 13 and 15 (i.e., a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2 and the nucleotide sequence of SEQ ID NO: 1) can be found in the specification, for example, at page 3, lines 27-30.

Support for element (c) of claims 13 and 15 (i.e., a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1) can be found at page 4, lines 2-4 of the disclosure. Support for the specifically recited stringent hybridizations conditions in element (c) of claims 13 and 15 can be found in the specification, for example, at page 6, lines 11-15.

Support for element (d) of claims 13 and 15 (*i.e.*, a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1 and which encodes a protein having PF1022 synthetase activity) can be found in the specification, for example, at page 6, lines 5-10.

Support for the method of culturing the host cell transformed with a vector containing the nucleic acid and expression of the nucleic acid of claim 13 can be found at page 4, lines 12-23, and page 20, line 3 to page 21, line 25.

VI. GROUND OF REJECTION TO BE REVIEWED ON APPEAL

Claims 13 and 15 were rejected under 35 U.S.C. § 112, first paragraph, on the basis that the specification is only enabling for the polypeptide of SEQ ID NO: 2 and a method for production thereof by culturing a host cell transformed with a vector comprising the nucleic acid of SEQ ID NO: 1 or a nucleic acid encoding SEQ ID NO: 2, and not for polypeptide variants encoded by nucleic acids that hybridize with SEQ ID NO: 1 under stringent conditions or nucleic acids that share at least 95% homology with SEQ ID NO: 1. See item 12 on pages 4-8 of the final Office Action dated October 16, 2005 and item 3 on pages 2-10 of the Advisory Action dated January 27, 2006.

VII. ARGUMENT

Claims 13 and 15 were rejected under 35 U.S.C. § 112, first paragraph, on the basis that the specification is only enabling for the polypeptide of SEQ ID NO: 2 and a method for production thereof by culturing a host cell transformed with a vector comprising the nucleic acid of SEQ ID NO: 1 or a nucleic acid encoding SEQ ID NO: 2, and not for polypeptide variants encoded by nucleic acids that hybridize with SEQ ID NO: 1 under stringent conditions or nucleic acids that share at least 95% homology with SEQ ID NO: 1. See item 12 on pages 4-8 of the final Office Action dated October 16, 2005 and item 3 on pages 2-10 of the Advisory Action dated January 27, 2006. Accordingly, the rejection is based on the premise that elements (c) and (d) of claims 13 and 15 are not enabled.

It is believed that the patentability of the invention is directed to the product of claim 15. In other words, the patentability of the process of claim 13 is based on the patentability of the product of claim 15.

Furthermore, it is respectfully submitted that elements (a), (b), (c) and (d) of claims 13 and 15 are each separately patentable from each other. As noted above, the rejection is based on the premise that elements (c) and (d) of claims 13 and 15 are not enabled. In fact, the Office has indicated that the claims are enabled for elements (a) and (b) of claims 13 and 15. If the rejection is affirmed in part on the basis that it remains applicable to elements (c) and (d), but not (a) and (b), kindly indicate such and provide Appellants an opportunity to amend the claims to that which is indicated as enabled.

On page 3 of the Advisory Action and on page 5 of the Office Action, it was indicated that the disclosure is limited to the single working example of SEQ ID NO: 2 and a method of making this polypeptide having PF1022 activity, because there is no working example of a variant of SEQ ID NO: 1 that encodes a polypeptide having PF1022 synthetase activity.

On pages 5-9 of the Advisory Action and on pages 6-7 of the final Office Action, it was indicated that the hybridization under stringent conditions language in part (c) and the "at least

95% homology" in part (d) of claims 13 and 15 are so broad as to encompass a vast number of nucleotide sequences encoding polypeptide variants having PF1022 synthetase activity.

This rejection is respectfully traversed for the same reasons set forth in the after final response filed January 4, 2006 and the response filed July 11, 2005 and for the following reasons.

The claims are directed to an isolated cyclic depsipeptide synthetase polypeptide having PF1022 activity and a method of making such.

Specifically, element (c) of claims 13 and 15 requires that the polypeptide is encoded by a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1 <u>under stringent conditions</u> at 0.2 x SSC concentration (1 x SSC: 15 mM trisodium citrate, 150 mM sodium chloride) in a 0.1 % SDS solution at 60°C for 15 minutes <u>and</u> which encodes a protein having PF1022 synthetase activity. Accordingly, the claims clearly define the specific stringent conditions required as set forth on page 6, lines 11-16 of the disclosure.

Element (d) of claims 13 and 15 requires that the polypeptide is encoded by a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1 and which encodes a protein having PF1022 synthetase activity.

In both cases, the claims require that the nucleotide sequence encode a functional protein with PF1022 synthetase activity.

As argued in the January 4, 2006 after final response and the July11, 2005 response, it is respectfully submitted that the polypeptides encompassed by claims 13 and 15 do <u>not</u> include the <u>vast number</u> of variant nucleotide sequences encoding polypeptide variants of SEQ ID NO:2 having PF1022 synthetase activity as asserted by the Office in the Advisory and the final Office Action. Moreover, even if the claims encompass a large number of polypeptides, it would not take undue experimentation to make and use the full scope of the claims.

Regarding the "hybridization under stringent conditions" and the "at least 95% homology language", Appellants again respectfully submit that PTO policy has long been to recognize that such language is patentable and enabled.

In this regard, and as discussed in prior responses, please note Examples 9, 10 and 14 of the PTO's Revised Interim Written Description Guidelines Training Materials, which were drafted and used by the PTO to train Examiners to comply with the Written Description Examination Guidelines in 66 Fed. Reg. 1099 (Jan. 5, 2001). Copies of Examples 9 and 10, which were attached to the July 11, 2005 response, are attached herewith along with Example 14.

On page 9 of the Advisory Action, the Office indicated that a discussion of the PTO's Written Description Examination Guidelines "appears to be misplaced" as they address the issue of written description and not enablement. However, this distinction was acknowledged in the last response. Moreover, as noted in the last response, the Examples and analysis in the Guidelines are instructive for the instant case even though the Guidelines deal with written description issues, as opposed to enablement. They are instructive for showing that PTO recognizes that the objected to claim language does <u>not</u> encompass the <u>vast number</u> of variants as asserted by the Office.

In Example 9, the claim is drawn to a genus of nucleic acids which hybridize under stringent conditions to a known DNA sequence, SEQ ID NO: 1, and encode a protein with a specific activity. There is a single species disclosed, i.e., SEQ ID NO: 1. Regarding the genus, it is clearly indicated that "a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent conditions set forth in the claims yield structurally similar DNAs." Based on this example, it is clear that the PTO recognizes that hybridization under stringent conditions language does <u>not</u> encompass the <u>vast number</u> of variants as asserted in the rejection.

In Example 10, the claims are drawn to a process for producing an isolated DNA that hybridizes under stringent conditions to a known sequence and to the DNA sequences which

hybridize to the known sequence. This Example is illustrative of the fact that the PTO has recognized that there is no substantial variation within such a genus, because hybridization under stringent conditions yields structurally similar molecules.

In Example 14 of the Guidelines, a claim to variants of a disclosed protein was found to be valid when the claim was limited to variant sequences that are at least 95% identical of the disclosed sequence and retain the functionality of the disclosed protein. The Guidelines' analysis of the example indicated that the procedures for making variants which have 95% identity and retain the functional activity are conventional in the art. It was also found that substantial variations among the members of the genus did not exist, because all the variants must possess the specified functional activity and must have at least 95% identity to the disclosed reference sequence. This Example shows that the PTO has recognized that "at least 95% identity" language does not encompass the vast number of variants as asserted in the rejection.

Elements (c) and (d) of the instant claims are analogous to the claims analyzed in the above-described examples. Moreover, as recognized by the PTO in these examples, it is respectfully submitted that a person of skill in the art would not expect substantial variation among the species encompassed within the scope of the claims, because the highly stringent conditions set forth in the claims and the 95% homology language yield structurally similar DNAs.

In addition, as discussed in the prior responses, the courts have also recognized that the instant claim language is patentable and enabled. Please take note of the following decisions Enzo Biochem, Inc. v. Gen-Probe Inc., 323 F.3d 956, 967, 63 USPQ2d 1609, 1613 (Fed. Cir. 2002) and Ex parte Herrmann, No. 2002-1630 (BPAI 2003), copies of which were attached to the July 11, 2005 response. Courtesy copies of these decisions are also attached herewith.

In Enzo, the Federal Circuit held that "[a]dequate written description may be present for a genus of nucleic acids based on their hybridization properties, 'if they hybridize under highly

stringent conditions to known sequences because such conditions dictate that all species within the genus will be structurally similar.'" Enzo, 323 F3d. at 956, 63 USPQ2d at 1615.

The Board in <u>Herrmann</u> dealt with similar issues for a claim directed to a genus of DNA that hybridize under stringent conditions. The Board found that polynucleotides encompassed by the claims directed to DNA that hybridize under stringent conditions to known DNA "do not include the 'potentially infinite number of variants'" as posited by the Examiner. <u>Herrmann</u>, page 17.

Although these cases deal with written description issues as opposed to enablement, they are instructive as evidence that the courts and the PTO recognize that there is no substantial variation within a claimed genus of sequences having "at least 95% homology" to a known sequence or sequences which "hybridize under stringent conditions", because such claim language yields <u>structurally similar</u> molecules and <u>excludes</u> the vast majority of variants.

In addition, the Board in Ex parte Bandman No. 2003-1805 (BPAI 2004) considered a similar question as to whether there was written description support for a polynucleotide "at least 90% identical" to a disclosed sequence. A copy of Bandman is attached herewith.

In <u>Bandman</u>, the Examiner rejected the claimed polynucleotide on the basis that the "at least 90% identical" language with no functional limitation lacked written description support, because the specification provided only a single representative species and purportedly did not provide guidance as to which specific nucleotide residues can tolerate change without affecting the functional activity of the polypeptide encoded thereby. See page 4, lines 29-30 of <u>Bandman</u>. The Board disagreed and found that claims directed to polynucleotide sequence at least 90% identical to a disclosed polynucleotide sequence met the written description requirement. In particular, the Board in <u>Bandman</u> held (page 6, lines 17-18) that two limitations, i.e., "at least 90% identity" and "naturally occurring", adequately described the genus of polynucleotides encompassed by claims 33 b) without that the claim further including a functional limitation.

Accordingly, the Board held that disclosure of a sequence with no functional language provided written support for the "at least 10%" variance in the disclosed polynucleotide.

Furthermore, please note that the claims in the present application recite a functional limitation of PF1022 synthetase activity, which provides more written support than was the case in <u>Bandman</u>.

In addition, it is noted that claim 8 in <u>Bandman</u> was <u>not</u> rejected by the Examiner for it contained both an identity limitation <u>and</u> a functional limitation. Kindly note that claims 13 and 15 of the instant application similarly recite both "at least 95% homology" language <u>and</u> the enzyme activity. In other words, claims 13 and 15 of the instant application include both a percent homology limitation and a functional limitation, similar to non-rejected claim 8 in <u>Bandman</u>. Accordingly, it is respectfully submitted that claims 13 and 15 should also <u>not</u> be rejected.

Although <u>Bandman</u> is non-precedential and deals with written description, as opposed to enablement, the decision is instructive as evidence that the PTO recognizes that substantial variation does <u>not</u> exist within a claimed genus of sequences having "at least 90% identity" to a known sequence. Moreover, the claims in the instant application recite "at least 95% identical", which has even less variance than was the case in <u>Bandman</u>.

Furthermore, it is scientifically well established in the art that the term "stringent conditions" refers to hybridization and washing under conditions that permit only binding of a nucleic acid molecule, such as an oligonucleotide or cDNA molecule probe, to <a href="https://high.night.n

As recognized by the courts and the PTO, hybridization under the specified stringent conditions of the claims require that the nucleotide sequence be <u>structurally similar</u> to the nucleotide sequence of SEQ ID NO:1. Moreover, by using stringent conditions, the "vast

number" of variant polynucleotides would be <u>excluded</u> from the claims. In fact, most variants would simply <u>not hybridize</u> to SEQ ID NO:1 under such conditions. Consequently, the claims are of a much narrower scope than, for example, hybridization under non-stringent conditions. Thus, in contrast to the position taken in the Office, the polypeptides encompassed by claims 13 and 15 do <u>not</u> include a <u>vast number</u> of polypeptide variants of SEQ ID NO:2 having PF1022 synthetase activity.

Moreover, even assuming arguendo that the claims encompass a large number of polypeptide variants, which they do not, it would <u>not take undue experimentation</u> to make and use the full scope of the claims.

It is well established that the test of enablement is whether one reasonably skilled in the art could make or use the invention based on the disclosure in the specification coupled with the knowledge in the art without undue experimentation. The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. The test is not whether any experimentation is necessary, but whether, if experimentation is necessary, it is undue. In fact, the test is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed. See M.P.E.P. § 2164.01.

The hybridization techniques and screening procedures disclosed in the specification are common and well known in the biotech industry as acknowledged by the PTO in Example 14 of the PTO's Written Description Guidelines. See the discussion above. As such, it would only require <u>routine</u> experimentation for the skilled artisan to isolate DNA that hybridizes under the specific stringent conditions of the claims to SEQ ID NO:1 or DNA that has at least 95% homology to SEQ ID NO:1, and then produce the polypeptide encoded by these sequences. Likewise, it would only require <u>routine</u> experimentation to then test the polypeptides encoded by such for the PF1022, cyclic depsipeptide synthetase activity. Even if doing so would require a

"considerable amount" of experimentation, Appellants respectfully submit that it would be routine and not undue. Again, the test for enablement is not merely quantitatively, since a considerable amount of experimentation is permissible, with respect to the direction in which to proceed.

Accordingly, it is respectfully submitted that it would <u>not</u> take undue experimentation to utilize the routine techniques disclosed in the specification and known in the art to isolate the limited number of DNA that hybridize under stringent conditions to SEQ ID NO:1, or have at least 95% homology thereto, and then express the nucleotides to obtain the polypeptides encoded thereby, and then further test the limited number of polypeptides encoded by these nucleotides for the requisite PF1022 activity.

As to the Office's concern regarding a lack of a working example of a variant nucleotide, it is well established that a specification need not contain an example if the invention is otherwise disclosed in such manner that one skilled in the art will be able to practice it without an undue amount of experimentation. See M.P.E.P. § 2164.02. Again, it would not take undue experimentation to make and use the full scope of the claimed invention for the reasons discussed above.

On pages 5-11 of the Advisory Action and on pages 6-7 of the final Office Action, it was indicated that the hybridization under stringent conditions language in part (c) and the "at least 95% homology" language in part (d) of claims 13 and 15 are so broad as to encompass a vast number of nucleotide sequences encoding polypeptide variants having PF1022 synthetase activity, because the hybridization under stringent conditions corresponds to 85% identity and the "at least 95% homology" corresponds to 19³²¹⁰ variants.

Appellants respectfully disagree with the interpretation and analysis in the Actions.

While it is acknowledged that the instant claim language may encompass a large number of potential variants, most of the genus would retain the functional activity of the disclosed protein. It is respectfully submitted that the instant claim language allows for variation which is

sufficiently predictive such that one skilled in the art could practice the invention without undue experimentation. More importantly, even if this would require a "considerable amount" of experimentation, Appellants respectfully submit that it would be <u>routine</u> and <u>not undue</u>.

Lastly, it is again respectfully submitted that this rejection conflicts with accepted practice at the PTO regarding "at least 95% homology" and hybridization under stringent conditions claim language. Many thousands of such claims appear in issued U.S. patents. Attached to the July 11, 2005 response were results of an online search of the PTO database for claim language containing "stringent conditions" to show that the PTO has allowed over a thousand patents with such claim language. Furthermore, attached herewith are results of an online search of the PTO database for the "at least 95% homology". Courtesy copies of these searches are attached herewith. These results also which show that the PTO has allowed thousands of patents with such claim language.

While it is acknowledged that patentability must be determined on a case-by-case basis, the results of the online search demonstrate that the PTO has long accepted such language in the claims. Thus, it appears that the rejection conflicts with a well accepted practice at the PTO. If the Board were to decide otherwise, such decision would call into question the validity of thousands of issued patents in the biotech industry.

For these reasons, the scope of enablement rejection under 35 U.S.C. § 112, first paragraph, of claims 13 and 15 is untenable and should be reversed.

VIII. CONCLUSION

For the foregoing reasons, the specification fully enables one of skill in the art to make and use the invention of claims 13 and 15 without undue experimentation. Thus, reversal of the final rejection is respectfully requested.

Attached herewith are a Claims Appendix, an Evidence Appendix, and a Related Proceedings Appendix.

This brief is submitted in triplicate with the requisite fee of \$500.00.

Respectfully submitted,

Naoki MIDOH et al.

y _

Registration No. 48,036

Attorney for Appellants

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CLAIMS APPENDIX

- 1. (Allowed) An isolated protein comprising the amino acid sequence of SEQ ID NO: 2.
- 2. (Withdrawn) A polynucleotide encoding the protein of claim 1.
- 3. (Withdrawn) A polynucleotide according to claim 2, which comprises the DNA sequence of SEQ ID NO: 1.
- 4. (Withdrawn) A polynucleotide selected from the group consisting of the following sequences:
 - (c) a DNA sequence of SEQ ID NO: 1,
- (d) a nucleotide sequence that has at least 70% homology to the DNA sequence of SEQ ID NO: 1 and encodes a protein having cyclic depsipeptide synthetase activity,
- (e) a modified DNA sequence of the DNA sequence of SEQ ID NO 1 that has one or more modifications selected from a substitution, a deletion, an addition and an insertion and encodes a protein having cyclic depsipeptide synthetase activity, and
- (f) a nucleotide sequence that hybridizes with the DNA sequence of SEQ ID NO: 1 under stringent conditions and encodes a protein having cyclic depsipeptide synthetase activity.
- 5. (Withdrawn) The polynucleotide according to claim 4, wherein sequence (d) is a nucleotide sequence that has at least 80% homology to the DNA sequence of SEQ ID NO: 1.
- 6. (Withdrawn) The polynucleotide according to claim 4, wherein sequence (d) is a nucleotide sequence that has at least 90% homology to the DNA sequence of SEQ ID NO: 1.

- 7. (Withdrawn) A recombinant vector comprising the polynucleotide of claim 2 or claim 4.
 - 8. (Withdrawn) A host comprising the expression vector of claim 7.
- 9. (Withdrawn) The host according to claim 8, which expresses a cyclic depsipeptide synthetase.
- 10. (Withdrawn) The host according to claim 8, which is a substance PF1022-producing microorganism.
- 11. (Withdrawn) A method for producing a cyclic depsipeptide, which comprises the steps of culturing the host of claim 8 and collecting the cyclic depsipeptide from the culture medium.
- 12. (Withdrawn) The method according to claim 11, wherein the cyclic depsipeptide is the substance PF1022 and a derivative thereof.

13. (Appealed) A method for producing a protein having cyclo(D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl-D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl) (PF1022) synthetase activity, which comprises the steps of:

culturing a host cell transformed with a vector containing a nucleotide sequence under conditions suitable for protein expression, wherein the nucleotide sequence is selected from the group consisting of:

- (a) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2;
- (b) the nucleotide sequence of SEQ ID NO: 1;
- (c) a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions at 0.2 x SSC concentration (1 x SSC: 15 mM trisodium citrate, 150 mM sodium chloride) in a 0.1 % SDS solution at 60°C for 15 minutes and which encodes a protein having PF1022 synthetase activity; and
- (d) a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1 and which encodes a protein having PF1022 synthetase activity; and collecting the protein from the culture medium.

14. (Cancelled)

- 15. (Appealed) An isolated protein encoded by a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2;
 - (b) the nucleotide sequence of SEQ ID NO: 1;
- (c) a nucleotide sequence that hybridizes with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions at 0.2 x SSC concentration (1 x SSC: 15 mM trisodium citrate, 150 mM sodium chloride) in a 0.1 % SDS solution at 60°C for 15 minutes and which encodes a protein having PF1022 synthetase activity; and
- (d) a nucleotide sequence that has at least 95% homology to the nucleotide sequence of SEQ ID NO: 1 and which encodes a protein having PF1022 synthetase activity.

16-17. (Cancelled)

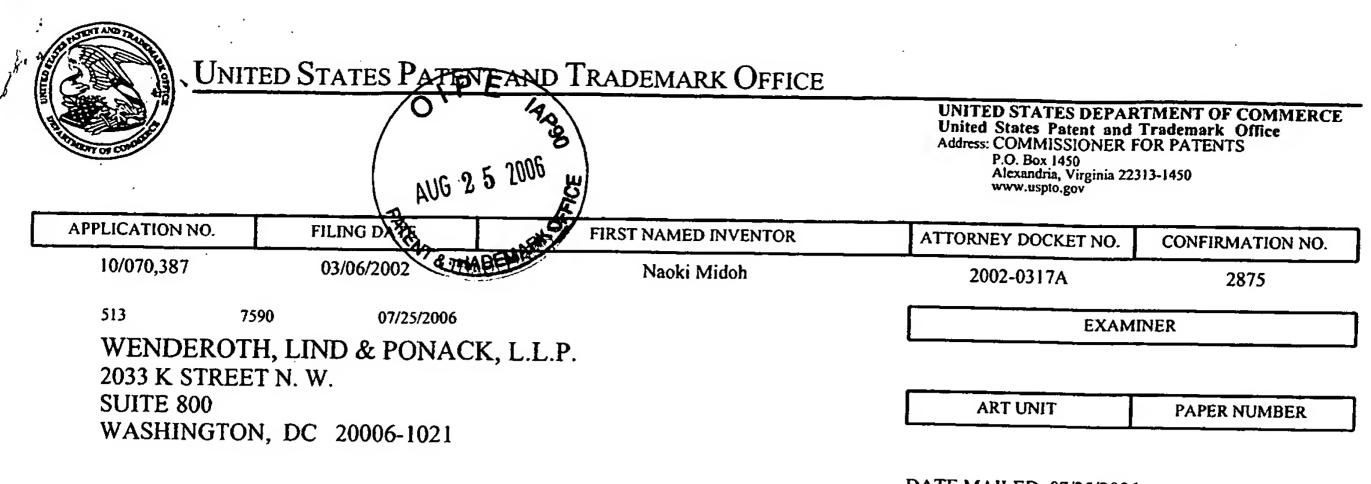
EVIDENCE APPENDIX

A) 4) 9 0

- 1. Examples 9, 10 and 14 of the PTO's Revised Interim Written Description
 Guidelines Training Materials, which were drafted and used by the PTO to train
 Examiners to comply with the Written Description Examination Guidelines in 66
 Fed. Reg. 1099 (Jan. 5, 2001);
- Enzo Biochem, Inc. v. Gen-Probe Inc., 323 F.3d 956, 63 USPQ2d 1609 (Fed. Cir. 2002) (please note that the proper citation for Enzo is 323 F.3d 956 and not 296 F.3d 1316 as cited in the previous responses);
- 3. Ex parte Herrmann, No. 2002-1630 (BPAI 2003);
- 4. Ex parte Bandman No. 2003-1805 (BPAI 2004);
- 5. Results of an online search of the PTO database for claim language containing "stringent conditions" which show that the PTO has allowed over a thousand patents with such claim language; and
- 6. Results of an online search of the PTO database for "at least 95% homology", which show that the PTO has allowed thousands of patents with such claim language.

RELATED PROCEEDINGS APPENDIX

NONE



DATE MAILED: 07/25/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

RECEIVED

JUL 26 2006

WENDEROTH, LIND & PONACK

<u></u>					<u></u>			
Notification of Non-Compliant Appeal Brief (37 CFR 41.37)		Application No.	8\	Applicant(s)				
		10/070,387	UG 2 5 2006 m	MIDOH ET AL.				
		Examiner \3	Æ/	Art Unit				
		Steadman, D	& MADEN MAN	1656				
-The MAILING DATE of this communication appears on the cover sheet with the correspondence address-								
The Appeal Brief filed on 30 June 2006 is defective for failure to comply with one or more provisions of 37 CFR 41.37.								
To avoid dismissal of the appeal, applicant must file anamended brief or other appropriate correction (see MPEP 1205.03) within ONE MONTH or THIRTY DAYS from the mailing date of this Notification, whichever is longer. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136.								
1. 🛛	The brief does not contain the items required under 37 CFR 41.37(c), or the items are not under the proper heading or in the proper order.							
2.	The brief does not contain a statement of the status of all claims, (e.g., rejected, allowed, withdrawn, objected to, canceled), or does not identify the appealed claims (37 CFR 41.37(c)(1)(iii)).							
3. 🗌	At least one amendment has been filed subsequent to the final rejection, and the brief does not contain a statement of the status of each such amendment (37 CFR 41.37(c)(1)(iv)).							
4.	(a) The brief does not contain a concise explanation of the subject matter defined in each of the independent claims involved in the appeal, referring to the specification by page and line number and to the drawings, if any, by reference characters; and/or (b) the brief fails to: (1) identify, for each independent claim involved in the appeal and for each dependent claim argued separately, every means plus function and step plus function under 35 U.S.C. 112, sixth paragraph, and/or (2) set forth the structure, material, or acts described in the specification as corresponding to each claimed function with reference to the specification by page and line number, and to the drawings, if any, by reference characters (37 CFR 41.37(c)(1)(v)).							
5. 🗌	The brief does not contain a concise statement of each ground of rejection presented for review (37 CFR 41.37(c)(1)(vi))							
6. 🗌	The brief does not present an argument under a separate heading for each ground of rejection on appeal (37 CFR 41.37(c)(1)(vii)).							
7. 🗌	The brief does not contain a correct copy of the appealed claims as an appendix thereto (37 CFR 41.37(c)(1)(viii)).							
8. 🔲	The brief does not contain copies of the evidence submitted under 37 CFR 1.130, 1.131, or 1.132 or of any other evidence entered by the examiner and relied upon by appellant in the appeal , along with a statement setting forth where in the record that evidence was entered by the examiner, as an appendix thereto (37 CFR 41.37(c)(1)(ix)).							
9. 🛛	The brief does not contain copies of the decisions rendered by a court or the Board in the proceeding identified in the Related Appeals and Interferences section of the brief as an appendix thereto (37 CFR $41.37(c)(1)(x)$).							
10.🛛								
	1.)Related proceedings appendix is inconsistent with the related appeals and interference section of the brief. If there are no such copies of decisions being submitted in the appeal, then the related appendix should be included with the indication "none".							
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				the Columbia (Cole) Appeal Specialist				